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Isabelle [BE/BE]; Rue du Centre 3, B-5170 Lesve (BE).
HAMELS, Sandrine [BE/BE]; Allée Saint Hubert 4,
B-6280 Loverval (BE).

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(74) Agents: **VAN MALDEREN, Joëlle** et al.; Place Reine
Fabiola 6/1, B-1083 Brussels (BE).

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(71) Applicant (*for all designated States except US*): **FAC-
ULTES UNIVERSITAIRES NOTRE-DAME DE LA
PAIX** [BE/BE]; Rue de Bruxelles 61, B-5000 Namur (BE).

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(72) Inventors; and

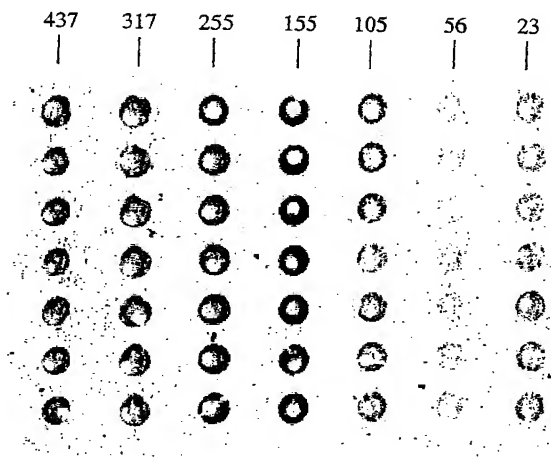
(75) Inventors/Applicants (*for US only*): **REMACLE,
José** [BE/BE]; Chemin des Pierres 14, B-5020 Mal-
onne (BE). **ZAMMATTEO, Nathalie** [BE/BE]; Avenue
Bourgmestre Jean Materne 202/3, B-5100 Jambes (BE).
DE LONGUEVILLE, Françoise [BE/BE]; Avenue Jean
Materne 110, B-5100 Jambes (BE). **ALEXANDRE,**

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(54) Title: METHOD AND KIT FOR THE SCREENING AND/OR THE QUANTIFICATION OF MULTIPLE HOMOLOGOUS
NUCLEIC ACID SEQUENCES ON ARRAYS



(57) Abstract: The present invention is related to a new detection and/or quantification method of a nucleotide sequence from other homologous sequences, and being present in a biological sample, comprising the steps of: amplifying or copying at least a part of original nucleotide sequences present in the biological sample into target nucleotide sequences; putting into contact the obtained target nucleotide sequences with corresponding capture nucleotide sequences bounded to an insoluble solid support, characterised in that said capture nucleotide sequences have a (single stranded) length comprised between about 40 and about 400 bases, and in that said capture nucleotide sequences are bounded to the insoluble support according to an array with a density of at least 5 different bound capture nucleotide sequences / cm² surface of solid support; and detecting and/or quantifying a signal resulting from the formation of double stranded nucleotide sequences resulting from the hybridisation by complementary base pairing.



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A. CLASSIFICATION OF SUBJECT MATTER

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B. FIELDS SEARCHED

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Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

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EPO-Internal, WPI Data, PAJ, MEDLINE, BIOSIS, EMBASE, CHEM ABS Data

C. DOCUMENTS CONSIDERED TO BE RELEVANT

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☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

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European Patent Office, P.B. 5818 Patentlaan 2
NL - 2280 HV Rijswijk
Tel. (+31-70) 340-2040, Tx. 31 651 epo nl,
Fax: (+31-70) 340-3016

Authorized officer

Mueller, F

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